

Db 13 TTTGAGAGATGAGAC 28

Search completed: May 15, 2001, 10:54:39

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2001, 10:05:34 ; Search time 1131.41 Seconds
(without alignments)
131.264 Million cell updates/sec

Title: US-09-373-230-5
Perfect score: 17
Sequence: 1 TTYGARGARATGAYCC 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

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3:	gb_est3:*
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232: em_gss_inv47:*
233: em_gss_inv48:*
234: em_gss_inv49:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	15.4	90.6	143	10	AA659492	AA659492 nu25d05.s
2	15.4	90.6	264	130	BB318243	BB318243 BB318243
3	15.4	90.6	327	1	AA054913	AA054913 SWAMCA150
C 4	15.4	90.6	335	156	T01405	T01405 WEST02126 E
C 5	15.4	90.6	375	118	AW673096	AW673096 ba57c02.y
6	15.4	90.6	434	4	AA237736	AA237736 mx29901.r
C 7	15.4	90.6	444	116	AW505386	AW505386 UI-HF-BNO
C 8	15.4	90.6	460	151	BF660764	BF660764 maa72e04.
C 9	15.4	90.6	474	16	AI121020	AI121020 ud69c02.x
C 10	15.4	90.6	499	173	BG076302	BG076302 H3158B03-
11	15.4	90.6	504	148	BF453847	BF453847 maa72e04.

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C 12 15.4 90.6 512 111 AM125102
13 15.4 90.6 564 173 BG088827
14 15.4 90.6 603 13 AA930362
15 15.4 90.6 648 12 AA842840
C 16 15.4 90.6 713 142 BE979995
17 15.4 90.6 719 136 BE544528
C 18 15.4 90.6 740 229 AG007422
19 15.4 90.6 772 169 BF793924
C 20 15.4 90.6 779 136 BE542842
21 15.4 90.6 872 223 AZ530862
C 22 15.4 90.6 921 231 CNS0447P
23 15.4 90.6 937 136 BE544857
C 24 15.4 84.7 252 119 AW741070
25 14.4 84.7 267 26 AV261563
C 26 14.4 84.7 279 121 AW930594
27 14.4 84.7 306 116 AW487887
28 14.4 84.7 325 114 AW356632
C 29 14.4 84.7 330 159 Z43844
30 14.4 84.7 342 148 BF461899
31 14.4 84.7 343 13 AA885264
32 14.4 84.7 351 102 A1836656
C 33 14.4 84.7 353 222 AZ498397
34 14.4 84.7 360 175 D37330
C 35 14.4 84.7 377 175 C45493
36 14.4 84.7 380 32 AM029991
C 37 14.4 84.7 396 103 A1866547
38 14.4 84.7 398 156 T09111
C 39 14.4 84.7 414 116 AW490430
40 14.4 84.7 423 2 AA107198
41 14.4 84.7 428 21 A1539998
42 14.4 84.7 429 2 AA140177
43 14.4 84.7 429 206 AQ434635
44 14.4 84.7 433 219 AZ318553
45 14.4 84.7 457 11 AA770992
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ALIGNMENTS

```

RESULT 1
AA659492/c
LOCUS
DEFINITION nu25d05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1209033, mRNA
sequence.
ACCESSION AA659492
VERSION AA659492.1 GI:2595646
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 143)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Mastron Linehan, M.D., Rodrigo Chuquai, M.D.
, Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 139.
FEATURES
source
1.143
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="IMAGE:1209033"
/clone_lib="NCI_CGAP_Pr2"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: pAMP10; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
```

```

BASE COUNT 54 a 25 c 23 g 41 t
ORIGIN
Query Match 90.6%; Score 15.4; DB 10; Length 143;
Best Local Similarity 76.5%; Pred. No. 6e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```

Oy 1 TTYGARGARATGAYCC 17
Db 52 TTTGAGCAGATGATGCC 36
```

```

RESULT 2
BB318243
LOCUS
DEFINITION BB318243 RIKEN full-length enriched, adult male corpora
quadrigemina Mus musculus cDNA clone B230373P10 3', mRNA sequence.
BB318243
ACCESSION BB318243
VERSION BB318243.1 GI:9025278
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 264)
AUTHORS Konno,H., Alzawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
,Y., Shigemoto,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya
,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshinide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermolabile enzymes by
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
```

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

Source

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/tissue_type="corpora quadrigemina"  
/dev_stage="adult"  
/lab_host="DH10B"
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BASE COUNT	72 a	44 c	52 g	96 t
ORIGIN				

Best Local Similarity 76.5%; Pred. No. 6.6e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 51 TTTGAGGAATGGATCC 67

AA054913

DEFINITION	SEQUENCE
SWAMCA1502SK Brugia malayi adult male cDNA (SAW94NL-BmAM) Brugia malayi cDNA clone SWAMCA1502 5', mRNA sequence.	<p>1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 </p>

SOURCE	Brugia malayi.
ORGANISM	Brugia malayi

Onchocercidae; Brugia.
1 (bases 1 to 327)

JOURNAL COMMENT unpublished (1995)
Contact: Steven A. Williams

Tel: 4135853826
Fax: 4135853786

FEATURES	Location/Qualifiers
source	1. .327

The library is available from Dr. S.A. Williams, email genome@smith.edu.

BASE COUNT	120 a	53 c	58 g	96 t
ORIGIN				

Best Local Similarity 76.5%; Pred. No. 6.8e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 225 TTCGAGGAGATGCATCC 241

T01405/c

elegans cDNA clone CEESQ49 similar to protein disulfide isomerase mRNA sequence.

SOURCE ORGANISM	Caenorhabditis elegans
Caenorhabditis elegans	

AUTHORS
McCombie, W.R., Kelley, J.M., Aubin, L., Goscoechea, M., Filtzgerald
, M.G., Wu, A., Adams, M.D., Dubnick, M., Kerlavage, A.R., Venter, J.C.

JOURNAL Unpublished (1993)
COMMENT Contact: Kerlavage, AR

Email: arkerlav@tiigr.org
Seq primer: M13 Forward.

FEATURES	Location/Qualifiers
source	1. .335

BASE COUNT	107 a	62 c	72 g	92 t	2 others
ORIGIN					

Best Local Similarity	76.5%;	Pred. No.	6.9e+02;
Matches	13;	Conservative	4;
		Mismatches	0;
		Indels	0;
		Gaps	0;

QY 1 TTYGARGARATGAYCC 17
11:11:11:1111:11
Db 313 TTGAGGAGATGATGCC 297

RESULT 5
AM673096/c 375 bp mRNA EST 11-APR-2000
LOCUS ba57c02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900642 5'
DEFINITION similar to TR:P78404 P78404 TRANSLATION REPRESSOR NAT1. [2]
TR:O60877 ;, mRNA sequence.

ACCESSION AM673096 GI:7538331
VERSION AM673096
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 375)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: ba57c02.x1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/lifresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 360.

FEATURES
source
1..375
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2900642"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."

BASE COUNT 129 a 74 c 66 g 105 t 1 others
ORIGIN

Query Match 90.6%; Score 15.4; DB 118; Length 375;
Best Local Similarity 76.5%; Pred. No. 7e+02; Indels 0; Gaps 0;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTYGARGARATGAYCC 17
11:11:11:1111:11
Db 279 TTGAGGAGATGATGCC 263

RESULT 6
AA237736 434 bp mRNA EST 03-MAR-1997
LOCUS mx29g01.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:681648 5'
DEFINITION similar to gb:D49949 Mouse mRNA for IGIF precursor polypeptide
(MOUSE);, mRNA sequence.

ACCESSION AA237736 GI:1861775
VERSION AA237736
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 434)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:421352
Putative full length read
vector to vector length is 437
Seq primer: -28m13 rev2 EP from Amersham.

FEATURES
source
1..434
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:681648"
/clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCGAATCTTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors.
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
constructed and normalized by Bento Soares and M.Fatima
Bonafido."

BASE COUNT 139 a 79 c 92 g 124 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 4; Length 434;
Best Local Similarity 76.5%; Pred. No. 7.1e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTYGARGARATGAYCC 17
11:11:11:1111:11
Db 82 TTGAGGAGATGATGCC 98

RESULT 7
AW505386/c 444 bp mRNA EST 02-MAR-2000
LOCUS UI-HF-BN0-alu-f-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
DEFINITION IMAGE:3080961 5', mRNA sequence.

ACCESSION AW505386 GI:7142970
VERSION AW505386
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 444)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source
Location/Qualifiers

1.444
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3080961"
/clone_lib="NIH_MGC_50"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 150 a 94 c 78 g 122 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 116; Length 444;
Best Local Similarity 76.5%; Pred. No. 7.2e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTYGARGARATGAYCC 17
11:11:11:11:11:11
Db 253 TTTGAGGAGATGATCC 237

RESULT 8
BF660764/c 460 bp mRNA EST 20-DEC-2000
LOCUS maa72e04.x1 Soares mouse 3NbMS Mus musculus CDNA clone
DEFINITION IMAGE:3822415 3' similar to SW:IL18_MOUSE P70380 INTERLEUKIN-18
PRECUSOR ; mRNA sequence.

ACCESSION BF660764 GI:11925898
VERSION BF660764
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 460)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other_ESTS: maa72e04.y1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1458767.

FEATURES
source
Location/Qualifiers

1.460
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3822415"
/clone_lib="Soares mouse 3NbMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA

was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCGCTGTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded CDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 130 a 96 c 84 g 150 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 151; Length 460;
Best Local Similarity 76.5%; Pred. No. 7.2e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTYGARGARATGAYCC 17
11:11:11:11:11:11
Db 357 TTTGAGGAATGATGCC 341

RESULT 9
A1121020/c 474 bp mRNA EST 02-SEP-1998
LOCUS ud69c02.x1 Sugano mouse liver mlia Mus musculus CDNA clone
DEFINITION IMAGE:1451138 3' similar to gb:D49949 Mouse mRNA for IGF precursor
polypeptide (MOUSE); mRNA sequence.

ACCESSION A1121020 GI:3521344
VERSION A1121020
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 474)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

JOURNAL The WashU-HMI Mouse EST Project
COMMENT Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:924454
Seq primer: custom primer used
High quality sequence stop: 410.

FEATURES
source
Location/Qualifiers

1.474
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1451138"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand CDNA
was primed with an oligo(dT) primer
[ATGTGGCCCTTTTCTTTTCTTTTCTTTT]; double-stranded CDNA was
ligated to a DraIII adaptor [TGTGGCCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library

constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGACACA."

BASE COUNT 132 a 97 c 83 g 162 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 16; Length 474;
Best Local Similarity 76.5%; Pred. No. 7.2e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTYGARGARATGAYCC 17
11:11:11:11:11:11
Db 364 TTTGAGGAAATGATCC 348

RESULT 10

BG076302/c 499 bp mRNA EST 26-JAN-2001
LOCUS
DEFINITION BG076302-3 NIA Mouse 15K CDNA Clone Set Mus musculus CDNA clone

H3158B03 3', mRNA sequence.

ACCESSION BG076302
VERSION BG076302.1 GI:12558871

KEYWORDS

SOURCE EST.

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 499)

AUTHORS Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka

, T.S., Carter, M.G. and Ko, M.S.H.

TITLE Verification and initial annotation of NIA mouse 15K CDNA clone set

JOURNAL Unpublished (2001)

COMMENT Other ESTs: H3158B03-5

Contact: George J. Kargul

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdnaelgusun.grc.nia.nih.gov

This clone set has been freely distributed to the community. Please

visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.

Plate: H3158 row: B column: 03

Seq primer: -21M13 Forward

High quality sequence stop: 499

POLYA=No.

FEATURES

Source

Location/Qualifiers

1..499

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="H3158B03"

/clone_lib="NIA Mouse 15K CDNA Clone Set"

/sex="Clones arrayed from a variety of CDNA libraries"

/dev_stage="Clones arrayed from a variety of CDNA

libraries"

/lab_host="DH10B"

/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This

clone is among a rearranged set of 15,247 clones from 11

embryo CDNA libraries (including preimplantation stage

embryos from unfertilized egg to blastocyst, embryonic

part of E7.5 embryos, extraembryonic part of E7.5 embryos

, and E12.5 female mesonephros/gonad) and one newborn

ovary CDNA library. Average insert size 1.5 kb. All

source libraries are cloned unidirectionally with Oligo(dT

) -Not primers. References include: (1) Genome-wide

expression profiling of mid-gestational placenta and embryo

using a 15,000 mouse developmental CDNA microarray, 2000,

Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)

Large-scale CDNA analysis reveals phased gene expression

patterns during preimplantation mouse development, 2000,

Development, 127: 1737-1749; (3) Genome-wide mapping of

unselected transcripts from extraembryonic tissue of

7.5-day mouse embryos reveals enrichment in the t-complex
and under-representation on the X chromosome, 1998, Hum
Mol Genet 7: 1967-1978."

BASE COUNT 131 a 107 c 96 g 165 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 173; Length 499;
Best Local Similarity 76.5%; Pred. No. 7.3e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTYGARGARATGAYCC 17
11:11:11:11:11:11
Db 243 TTTGAGGAAATGATCC 227

RESULT 11

BF453847

LOCUS

DEFINITION

BF453847

VERSION

KEYWORDS

SOURCE EST.

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 504)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:1458767

Seq primer: -40RP from Gibco

High quality sequence stop: 468.

Location/Qualifiers

1..504

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:3822415"

/clone_lib="Soares mouse 3NbMS"

/sex="male"

/tissue_type="Spleen"

/dev_stage="4 weeks"

/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA

was primed with a Not I - oligo(dT) primer (5'

TGTACCAATCTGAAGTGGAGCGCGCGCTTTT TTT TTT TTT TTT TTT TTT

3')]; double-stranded CDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. RNA

provided by Dr. Bertrand Jordan. Library went through

three rounds of normalization, and was constructed by

Bento Soares and M.Fatima Bonaldo."

BASE COUNT 164 a 96 c 105 g 138 t 1 others

ORIGIN

Query Match 90.6%; Score 15.4; DB 148; Length 504;
Best Local Similarity 76.5%; Pred. No. 7.3e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTYGARGARATGAYCC 17
11:11:11:11:11:11

Db 147 TTTGAGGAATGCATCC 163

RESULT 12
 AM125102/c
 LOCUS
 DEFINITION AM125102 512 bp mRNA EST 22-OCT-1999
 UI-M-BH2.1-apx-g-10-0-UI.S1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone
 UI-M-BH2.1-apx-g-10-0-UI 3', mRNA sequence.
 AM125102
 AM125102.1 GI:6100632
 EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 512)
 TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL
 MEDLINE Genome Res. 6 (9), 791-806 (1996)
 COMMENT 97044477
 Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: MEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to identify it as a clone from the
 normalized basal ganglia library cDNA Library Preparation: M.B.
 Soares lab Clone distribution: NIH BMAP cDNA clones will be made
 available by the means that is soon to be determined. When NIH
 determines the means for distribution of the BMAP cDNA clones, this
 record will be updated accordingly when that means is determined.
 The following repetitive elements were found in this cDNA sequence:
 17-81, >MSTD#LTR/MalR
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES
 source

Location/Qualifiers
 1..512
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH2.1-apx-g-10-0-UI"
 /clone_lib="NIH_BMAP_M.S3.1"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The
 NIH_BMAP_M.S3.1 library is a subtracted library of a
 series, ultimately derived from a mixture of individually
 tagged normalized libraries from ten regions of the mouse
 brain (cerebellum, brain stems, olfactory bulbs,
 hypothalamus, cortex, amygdala, basal ganglia, pineal
 gland, striatum, hippocampus) after a series of
 subtractions to reduce the representation of cDNAs from
 which ESTs had already been generated. The following
 serially subtracted libraries were generated in this
 process: NIH_BMAP_M.S3.1, NIH_BMAP_M.S2, NIH_BMAP_M.S1.
 The subtracted library (NIH_BMAP_M.S3.1) was constructed
 as follows: PCR amplified cDNA inserts from NIH_BMAP_M.S2
 clones from which 3' ESTs had been derived was used as a
 driver in a hybridization with the NIH_BMAP_M.S2 library
 in the form of single-stranded circles. The remaining
 single-stranded circles (subtracted library) was purified
 by hydroxyapatite column chromatography, converted to
 double-stranded circles and electroporated into DH10B
 bacteria (Life Technologies) to generate the
 NIH_BMAP_M.S3.1 library. This procedure has been

previously described (Bonaldo, Lennon and Soares, Genome
 Research 6:791-806, 1996)
 TAG_LIB=NIH_BMAP_M.S3.1
 TAG_TISSUE=basal-ganglia
 TAG_SEQ=GTGAC"

BASE COUNT 135 a 104 c 94 g 179 t
 ORIGIN

Query Match 90.6%; Score 15.4; DB 111; Length 512;
 Best Local Similarity 76.5%; Pred. No. 7.3e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTYGARGARATGAYCC 17
 11:11:11:11:11:11
 Db 374 TTTGAGGAATGCATCC 358

RESULT 13
 BG088827
 LOCUS
 DEFINITION BG088827 564 bp mRNA EST 26-JAN-2001
 H3158B03-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
 H3158B03 5', mRNA sequence.
 BG088827
 BG088827.1 GI:12571391
 EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 564)
 TITLE Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
 'T.S., Carter,M.G. and Ko,M.S.H.
 Verification and initial annotation of NIA mouse 15K cDNA clone set
 Unpublished (2001)
 JOURNAL Other_ESTS: H3158B03-3
 COMMENT Contact: George J. Kargul
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.
 Plate: H3158 row: B column: 03
 Seq primer: -21M13 Reverse
 High quality sequence stop: 564
 POLYA=No.

FEATURES
 source

Location/Qualifiers
 1..564
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="H3158B03"
 /clone_lib="NIA Mouse 15K cDNA Clone Set"
 /sex="Clones arrayed from a variety of cDNA libraries"
 /dev_stage="Clones arrayed from a variety of cDNA
 libraries"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
 clone is among a rearrayed set of 15,247 clones from 11
 embryo cDNA libraries (including preimplantation stage
 embryos from unfertilized egg to blastocyst, embryonic
 part of E7.5 embryos, extraembryonic part of E7.5 embryos
 , and E12.5 female mesonephros/gonad) and one newborn
 ovary cDNA library. Average insert size 1.5 kb. All
 source libraries are cloned unidirectionally with Oligo(dT
)-Not primers. References include: (1) Genome-wide
 expression profiling of mid-gestation placenta and embryo
 using a 15,000 mouse developmental cDNA microarray, 2000,
 Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
 Large-scale cDNA analysis reveals phased gene expression
 patterns during preimplantation mouse development, 2000,
 Development, 127: 1737-1749; (3) Genome-wide mapping of

unselected transcripts from extraembryonic tissue of
7.5-day mouse embryos reveals enrichment in the t-complex
and under-representation on the X chromosome, 1998, Hum
Mol Genet 7: 1967-1978."

BASE COUNT 187 a 111 c 115 g 151 t

ORIGIN

Query Match 90.6%; Score 15.4; DB 173; Length 564;
Best Local Similarity 76.5%; Pred. No. 7.4e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTYGARGARATGAYCC 17
||:||||:||||:|
Db 246 TTTCAGGAAATGATCC 262

RESULT 14
AA930362

LOCUS 603 bp mRNA EST 23-APR-1998
DEFINITION vs59f07.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:1150597 5' similar to gb:D49949 Mouse mRNA for IGF1 precursor
polypeptide (MOUSE);, mRNA sequence.

ACCESSION
AA930362

VERSION AA930362.1 GI:3079955

KEYWORDS

SOURCE

ORGANISM

house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 603)

REFERENCE

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE

JOURNAL

COMMENT

The Washu-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washu-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:623805
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 445.

FEATURES

SOURCE

1. 603
/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1150597"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'"

BASE COUNT 197 a 111 c 132 g 163 t

ORIGIN

Query Match 90.6%; Score 15.4; DB 13; Length 603;
Best Local Similarity 76.5%; Pred. No. 7.5e+02;

Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTYGARGARATGAYCC 17
||:||||:||||:|
Db 248 TTTCAGGAAATGATCC 264

RESULT 15

AA842840

LOCUS 648 bp mRNA EST 03-MAR-1998

DEFINITION SWAMCAC03E10SK Brugia malayi adult male cDNA (SAW94NL-BmAM) Brugia

malayi cDNA clone SWAMCAC03E10 5', mRNA sequence.

ACCESSION
AA842840

VERSION AA842840.1 GI:2924177

KEYWORDS

SOURCE

ORGANISM

Brugia malayi.
Brugia malayi.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Williams, S.A.
Genes expressed in adult males of Brugia malayi
Unpublished (1995)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers

FEATURES

SOURCE

1. 648
/organism="Brugia malayi"
/strain="TRS Labs"
/db_xref="taxon:6279"
/clone="SWAMCAC03E10"
/clone_lib="Brugia malayi adult male cDNA (SAW94NL-BmAM)"
/lab_host="XLI-Blue MRF"
/note="Vector: lambda UniZap XR; Site_1: EcoRI; Site_2:
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from adult males of Brugia malayi
isolated from jirds and converted to double stranded cDNA
using reverse transcriptase and oligo(dT) followed by
RNase H and DNAPol I. The library had 4.6 x 10E6
independent recombinants and average insert size was 800
base pairs. The library was constructed by Noelle Ling.
The library is available from Dr. S.A. Williams, email
genome@smith.edu."

BASE COUNT 236 a 95 c 114 g 200 t 3 others

ORIGIN

Query Match 90.6%; Score 15.4; DB 12; Length 648;
Best Local Similarity 76.5%; Pred. No. 7.6e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTYGARGARATGAYCC 17
||:||||:||||:|
Db 544 TTTCAGGAGATGATCC 560

RESULT 16

BE979995

LOCUS 713 bp mRNA EST 05-OCT-2000

DEFINITION BE979995

UI-M-BG2-bcp-h-09-0-UI.s1 NIH BMAP_MSC_S1 Mus musculus cDNA clone

UI-M-BG2-bcp-h-09-0-UI 3', mRNA sequence.

ACCESSION
BE979995

VERSION BE979995.1 GI:10647511

KEYWORDS

SOURCE

ORGANISM

house mouse.
Mus musculus

REFERENCE 1 (bases 1 to 713)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the basal ganglia tissue cDNA Library Preparation: M.B. Soares lab
Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 17-81,
>MSTD#LTR/MaLR
Seq primer: M13 Forward
POLYA=yes.

FEATURES
source location/Qualifiers
1..713
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BG2-bcp-h-09-0-UI"
/clone_lib="NIH_BMAP_MSC_S1"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_MSC_S1 library is a subtracted library derived NIH_BMAP_MSC_N. NIH_BMAP_MSC_N was made from mouse spinal cord tissue. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu.
TAG_LIB=NIH_BMAP_MSC_S1
TAG_TISSUE=Basal-ganglia
TAG_SEQ=TGTAC"

BASE COUNT 189 a 144 c 135 g 245 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 142; Length 713;
Best Local Similarity 76.5%; Pred. No. 7.7e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTYGARGARATGAYCC 17
||:|:|:|:|:|:|:|:|:|
Db 374 TTTGAGGAATGATCC 358

RESULT 17
BE544528/c 719 bp mRNA EST 09-AUG-2000
LOCUS BE544528
DEFINITION 601078354F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464221 5',
mRNA sequence.
ACCESSION BE544528
VERSION BE544528.1 GI:9773173
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 719)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM8464 row: 1 column: 14
High quality sequence stop: 518.

FEATURES
source location/Qualifiers
1..719
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3464221"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."

BASE COUNT 229 a 155 c 148 g 187 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 136; Length 719;
Best Local Similarity 76.5%; Pred. No. 7.7e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTYGARGARATGAYCC 17
||:|:|:|:|:|:|:|:|:|
Db 321 TTTGAGGAGATGATCC 305

RESULT 18
AG007422/c 740 bp DNA GSS 07-FEB-1999
LOCUS AG007422
DEFINITION Homo sapiens genomic DNA, 21q region, clone: T1539X36, genomic survey sequence.
ACCESSION AG007422
VERSION AG007422.1 GI:3097375
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone:T1539X36.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (29-APR-1998) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan
(E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
Fax:0427-78-9561)
2 (bases 1 to 740)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in Database (1998) In press

FEATURES
source location/Qualifiers
1..740
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/clone="T1539X36"
/map="21q"

```
BASE COUNT      182 a      168 c      167 g      208 t      15 others
ORIGIN

Query Match
Best Local Similarity 90.6%; Score 15.4; DB 229; Length 740;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTYGARGARATGCAYCC 17
        ||:|:|:|:|:|:|:|:|:|
Db      285 TTGAGGAAATGATGCC 269

RESULT 19
BF793924/c      772 bp      mRNA      EST      12-JAN-2001
LOCUS
DEFINITION      602254534F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4346816 5',
ACCESSION      BF793924
VERSION      BF793924.1 GI:12098978
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 772)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Tel: (301) 496-1550
              Email: Robert_Strausberg@nih.gov
              Tissue Procurement: ATCC
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.llnl.gov
              Plate: LLM9969 row: c column: 09
              High quality sequence stop: 710.
              Location/Qualifiers
                1..772
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:4346816"
                  /clone_lib="NIH_MGC_84"
                  /tissue_type="adrenal cortex carcinoma, cell line"
                  /lab_host="DH10B (phage-resistant)"
                  /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
                  NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
                  primed. Average insert size 1.229 kb. Library enriched for
                  full-length clones and constructed by Life Technologies.
                  Note: this is a NIH_MGC library."

BASE COUNT      265 a      155 c      149 g      203 t
ORIGIN

Query Match
Best Local Similarity 90.6%; Score 15.4; DB 169; Length 772;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTYGARGARATGCAYCC 17
        ||:|:|:|:|:|:|:|:|:|
Db      172 TTGAGGAGATGATGCC 156

RESULT 20
BE542842/c      779 bp      mRNA      EST      09-AUG-2000
LOCUS
DEFINITION      601067660F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453758 5',
ACCESSION      BE542842
mRNA sequence.

BASE COUNT      182 a      168 c      167 g      208 t      15 others
ORIGIN

VERSION      BE542842.1 GI:9771487
EST.
KEYWORDS      human.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 779)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Tel: (301) 496-1550
              Email: Robert_Strausberg@nih.gov
              Tissue Procurement: ATCC
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: Incyte Genomics, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.llnl.gov
              Plate: LLM8437 row: h column: 15
              High quality sequence stop: 657.
              Location/Qualifiers
                1..779
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3453758"
                  /clone_lib="NIH_MGC_10"
                  /cell_line="MGC36"
                  /lab_host="DH10B"
                  /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                  Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                  Average insert size 1.5 kb. Library prepared by Life
                  Technologies."

BASE COUNT      245 a      170 c      160 g      204 t
ORIGIN

Query Match
Best Local Similarity 90.6%; Score 15.4; DB 136; Length 779;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTYGARGARATGCAYCC 17
        ||:|:|:|:|:|:|:|:|:|
Db      134 TTGAGGAGATGATGCC 118

RESULT 21
AZ530862/c      872 bp      DNA      GSS      03-NOV-2000
LOCUS
DEFINITION      ENTAC19TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
ACCESSION      AZ530862
VERSION      AZ530862.1 GI:11085052
KEYWORDS      GSS.
SOURCE      Entamoeba histolytica.
ORGANISM      Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE      1 (bases 1 to 872)
AUTHORS      Loftus B., Van Aken, S. and Fraser, C.
TITLE      Determination of clone end sequences from Entamoeba histolytica
JOURNAL      HMI:IMSS sheared DNA library
COMMENT      Unpublished (2000)
              Contact: Brendan J Loftus
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 0200
              Fax: 301 838 0208
              Email: bjlloftus@tigr.org
              Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
              DNA library
              Seq primer: M13-Reverse
```

Class: shotgun
High quality sequence start: 62
High quality sequence stop: 727.
Location/Qualifiers
1. .872
/organism="Entamoeba histolytica"
/strain="HML:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica sheared DNA"
/note="Vector: PHOS1; Site_1: Bst I; Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Borell, Oxford University Press, 1999)."

BASE COUNT 316 a 120 c 153 g 277 t 6 others

ORIGIN

Query Match 90.6%; Score 15.4; DB 223; Length 872;
Best Local Similarity 76.5%; Pred. No. 7.9e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTYGARGARATGAYCC 17
11:11:11:11:11:11
Db 783 TTTGAGAGATGATCC 767

RESULT 22
CNS0447P/c 921 bp DNA GSS 18-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 081E03 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL273742
VERSION AL273742.1 GI:7996005
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 921)
AUTHORS Roest-Crollius, H., Jallou, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 921)
AUTHORS Roest-Crollius, H., Jallou, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 921)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
source
Location/Qualifiers
1. .921
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="081E03"
/clone_lib="G"
/note="Genoscope sequence ID : COB081AC02LP1-end : T7"

BASE COUNT 224 a 199 c 220 g 273 t 5 others

ORIGIN

Query Match 90.6%; Score 15.4; DB 231; Length 921;
Best Local Similarity 76.5%; Pred. No. 8e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTYGARGARATGAYCC 17
11:11:11:11:11:11
Db 682 TTTGAGAGATGATCC 666

RESULT 23
BE544857/c 937 bp mRNA EST 09-AUG-2000
LOCUS 601078856P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464700 5',
DEFINITION mRNA sequence.
ACCESSION BE544857
VERSION BE544857.1 GI:9773502
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 937)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM8465 row: p column: 13
High quality sequence stop: 683.
Location/Qualifiers
1. .937
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3464700"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/note="Organ: cervix; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

BASE COUNT 306 a 202 c 196 g 233 t

ORIGIN

Query Match 90.6%; Score 15.4; DB 136; Length 937;
Best Local Similarity 76.5%; Pred. No. 8e+02;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTYGARGARATGAYCC 17
11:11:11:11:11:11
Db 637 TTTGAGAGATGATCC 621

RESULT 24
AW741070/c 252 bp mRNA EST 27-APR-2000
LOCUS
DEFINITION ug94d12.y1 NCI_CGAP_Mam10 Mus musculus cDNA clone IMAGE:2938775 5',
mRNA sequence.
ACCESSION
VERSION AW741070
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 252)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT Unpublished (1997)
Other_ESTRs: ug94d12.x1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Jeffrey Green M.D.,
Gilbert Smith, Ph.D., William Muller, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULIN)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ULIN at:
image.llnl.gov/image/html/iresources.shtml
MGI:1051195
Seq primer: -40RP from Gibco
High quality sequence stop: 249.
FEATURES
source
1..252
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:2938775"
/clone_1ib="NCI_CGAP_Mam10"
/tissue_type="pooled mammary gland tumors"
/lab_host="DH10B (phage-resistant)"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: NotI; Site_2: EcoRI;
1st strand cDNA was prepared from mRNA obtained from
pooled mammary gland tumors with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCCACTAGTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 79 a 45 c 52 g 76 t
ORIGIN
Query Match 84.7%; Score 14.4; DB 119; Length 252;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 2 TYGARGARATGGAYCC 17
|:|:|:|:|:|:|:|:|:|
Db 138 TTGAAGAAATGACCC 123
RESULT 25
AV261563 267 bp mRNA EST 04-NOV-1999
LOCUS
DEFINITION AV261563 RIKEN full-length enriched, adult male testis (DH10B) Mus
musculus cDNA clone 4930422M09 3', mRNA sequence.
ACCESSION
VERSION AV261563.1 GI:6249022

KEYWORDS
SOURCE EST.
ORGANISM house mouse.
MUS musculus
REFERENCE
1 (bases 1 to 267)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai
,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata
,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,
Suzuki,H., Takahashi,F., Tateo,M., Tomimaga,N., Tsunoda,Y.,
Watabiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,
Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al. 1999)
JOURNAL
COMMENT Unpublished (1999)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:<http://genome.rtc.riken.go.jp/>
Sasaki,N., Izawa,M., Watabiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Katsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.
FEATURES
source
1..267
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930422M09"
/clone_1ib="RIKEN full-length enriched, adult male testis
(DH10B)"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTVN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
BASE COUNT 51 a 69 c 75 g 72 t
ORIGIN

Query Match 84.7%; Score 14.4; DB 26; Length 267;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTYGARGARATGGAYC 16
|:|:|:|:|:|:|:|:|:
DB 13 TTTGAGGAGATGGACC 28

Search completed: May 15, 2001, 10:54:39
Job time: 2945 sec